



CIBT-P01-130SequenceListing
SEQUENCE LISTING

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<120> BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING

<130> CIBT-P01-130

<140> 09/558,741

<141> 2000-04-26

<150> 07/831,967

<151> 1992-02-06

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<223> 741F8 sFv'

<220>

<221> CDS

<222> (3)..(752)

<223>

<400> 1

cc atg gcg gag atc caa ttg gtg cag tct gga cct gag ctg aag aag 47

Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys

1

5

10

15

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc 95

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe

20

25

30

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta 143

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu

35

40

45

aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct 191

Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala

50

55

60

gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc 239

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser

65

70

75

act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca 287

Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr

80

85

90

95

tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg 335

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Tyr	Phe	Cys	Gly	Arg	Gln	Phe	Ile	Thr	Tyr	Gly	Gly	Phe	Ala	Asn	Trp		
				100					105					110			
ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	tcg	agc	tcc	tcc	gga	tct	383	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ser	Ser	Ser	Ser	Gly	Ser		
			115					120					125				
tca	tct	agc	ggg	tcc	agc	tcg	agc	gat	atc	gtc	atg	acc	cag	tct	cct	431	
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro		
		130					135					140					
aaa	ttc	atg	tcc	acg	tca	gtg	gga	gac	agg	gtc	agc	atc	tcc	tgc	aag	479	
Lys	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Ser	Cys	Lys		
	145					150					155						
gcc	agt	cag	gat	gtg	agt	act	gct	gta	gcc	tgg	tat	caa	caa	aaa	cca	527	
Ala	Ser	Gln	Asp	Val	Ser	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro		
					165					170					175		
ggg	caa	tct	cct	aaa	cta	ctg	att	tac	tgg	aca	tcc	acc	cgg	cac	act	575	
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Thr	Ser	Thr	Arg	His	Thr		
				180					185					190			
gga	gtc	cct	gat	cgc	ttc	aca	ggc	agt	gga	tct	ggg	aca	gat	tat	act	623	
Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr		
			195					200					205				
ctc	acc	atc	agc	agt	gtg	cag	gct	gaa	gac	ctg	gca	ctt	cat	tac	tgt	671	
Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Leu	His	Tyr	Cys		
		210				215						220					
cag	caa	cat	tat	aga	gtg	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg	719	
Gln	Gln	His	Tyr	Arg	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu		
	225					230					235						
gag	ata	aaa	cgg	gct	gat	ggg	gga	ggg	gga	tgt	taac	ggggga	ggg	ggat	ggt	772	
Glu	Ile	Lys	Arg	Ala	Asp	Gly	Gly	Gly	Gly	Cys							
	240				245					250							
gggtctcgtt	acgttgcgga	tctcgaggct	atctttacta	actctttaccg	taaagttctg											832	
gctcaactgt	ctgcacgcaa	gcttttgcag	gatatcatga	gcgcttaaga	tccgtcgacc											892	
tgcaggcatg	caagctt															909	

<210> 2
 <211> 250
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 741F8 sFv'

<400> 2

Met	Ala	Glu	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro
1				5					10					15	

Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
			20					25					30		

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Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
 35 40 45
 Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu
 50 55 60
 Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr
 65 70 75 80
 Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr
 85 90 95
 Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
 115 120 125
 Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
 130 135 140
 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
 145 150 155 160
 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
 165 170 175
 Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
 180 185 190
 Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
 195 200 205
 Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
 210 215 220
 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 225 230 235 240
 Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
 245 250

<210> 3
 <211> 779
 <212> DNA
 <213> Artificial Sequence

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<220>
 <223> 26-10 sFv'
 <220>
 <221> CDS
 <222> (3)..(758)
 <223>

<400> 3
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 Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
 1 5 10 15
 ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc 95
 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr
 20 25 30
 gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac 143
 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp
 35 40 45
 tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag 191
 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln
 50 55 60
 aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act 239
 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
 65 70 75
 gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac 287
 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
 80 85 90 95
 tat tgc gcg ggc tcc tct ggt aac aaa tgg gcc atg gat tat tgg ggt 335
 Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly
 100 105 110
 cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt 383
 His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly
 115 120 125
 tcc agc tcg agt gga tcc gac gtc gta atg acc cag act ccg ctg tct 431
 Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser
 130 135 140
 ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc cgc tct tcc 479
 Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
 145 150 155
 cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg 527
 Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
 160 165 170 175
 caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac 575
 Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn
 180 185 190
 cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act 623
 Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205
 gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc 671
 Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile

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210 215 220
 tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc 719
 Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly
 225 230 235
 acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc 768
 Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
 240 245 250
 ccgggggatc c 779

<210> 4
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 26-10 sFv'

<400> 4

Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
 1 5 10 15

Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp
 20 25 30

Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr
 35 40 45

Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
 85 90 95

Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
 100 105 110

Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
 115 120 125

Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
 130 135 140

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
 145 150 155 160

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Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
 165 170 175

Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr
 210 215 220

Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
 225 230 235 240

Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
 245 250

<210> 5
 <211> 739
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 520C9 sFv

<220>
 <221> CDS
 <222> (1)..(729)
 <223>

<400> 5
 gag atc caa ttg gtg cag tct gga cct gag ctg aag aag cct gga gag 48
 Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat 96
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
 20 25 30

gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg 144
 Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc 192
 Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
 50 55 60

aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat 240
 Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
 65 70 75 80

ttg cag atc aac aac ctc aga aat gag gac tcg gcc aca tat ttc tgt 288
 Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys

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85

90

95

gca	aga	cga	ttt	ggg	ttt	gct	tac	tgg	ggc	caa	ggg	act	ctg	gtc	agt	336
Ala	Arg	Arg	Phe	Gly	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ser	
			100					105					110			
gtc	tct	gca	tcg	ata	tcg	agc	tcc	tcc	gga	tct	tca	tct	agc	ggg	tcc	384
Val	Ser	Ala	Ser	Ile	Ser	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Gly	Ser	
		115					120					125				
agc	tcg	agt	gga	tcc	gat	atc	cag	atg	acc	cag	tct	cca	tcc	tcc	tta	432
Ser	Ser	Ser	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	
		130				135					140					
tct	gcc	tct	ctg	gga	gaa	aga	gtc	agt	ctc	act	tgt	cgg	gca	agt	cag	480
Ser	Ala	Ser	Leu	Gly	Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	
					150					155					160	
gac	att	ggg	aat	agc	tta	acc	tgg	ctt	cag	cag	gaa	cca	gat	gga	act	528
Asp	Ile	Gly	Asn	Ser	Leu	Thr	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	
				165					170					175		
att	aaa	cgc	ctg	atc	tac	gcc	aca	tcc	agt	tta	gat	tct	ggg	gtc	ccc	576
Ile	Lys	Arg	Leu	Ile	Tyr	Ala	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	
			180					185					190			
aaa	agg	ttc	agt	ggc	agt	cgg	tct	ggg	tca	gat	tat	tct	ctc	acc	atc	624
Lys	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	
		195					200					205				
agt	agc	ctt	gag	tct	gaa	gat	ttt	gta	gtc	tat	tac	tgt	cta	caa	tat	672
Ser	Ser	Leu	Glu	Ser	Glu	Asp	Phe	Val	Val	Tyr	Tyr	Cys	Leu	Gln	Tyr	
		210				215				220						
gct	att	ttt	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aac	ctg	gaa	ata	aaa	720
Ala	Ile	Phe	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Asn	Leu	Glu	Ile	Lys	
					230					235					240	
cgg	gct	gat	taatctgcag													739
Arg	Ala	Asp														

<210> 6
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 520C9 sFV

<400> 6

Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
 20 25 30

Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

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Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
50 55 60

Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
65 70 75 80

Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser
100 105 110

Val Ser Ala Ser Ile Ser Ser Ser Gly Ser Ser Ser Gly Ser
115 120 125

Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln
145 150 155 160

Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr
165 170 175

Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro
180 185 190

Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile
195 200 205

Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr
210 215 220

Ala Ile Phe Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys
225 230 235 240

Arg Ala Asp

<210> 7
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Linker 1

<400> 7

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 8
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 2

<400> 8

Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly
1 5 10 15

<210> 9
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal tail

<400> 9

Ser Cys
1

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal tail

<400> 10

Gly Gly Gly Gly Cys
1 5

<210> 11
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal tail

<400> 11

His His His His His Gly Gly Gly Gly Cys
1 5 10

<210> 12
<211> 118
<212> PRT
<213> Mus musculus

<400> 12

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Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Glu Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Thr Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe
65 70 75 80

Asn Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Lys
115

<210> 13
<211> 120
<212> PRT
<213> Mus musculus

<400> 13

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp Phe
20 25 30

Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr Ile
35 40 45

Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

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Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His Gly
100 105 110

Ala Ala Ser Val Thr Val Ser Ser
115 120

<210> 14
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid peptide

<400> 14

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile His Trp Leu Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Cys Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly His Gly Ala Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 15
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid peptide

<400> 15

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile His Trp Leu Lys Gln Pro Pro Gly Arg Leu Glu Trp Ile Gly
35 40 45

Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe Lys
50 55 60

Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Tyr Thr His Tyr Tyr Phe
100

<210> 16
<211> 118
<212> PRT
<213> Mus musculus

<400> 16

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Ser Asn Asp
20 25 30

Tyr Tyr Thr Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Val Phe Tyr His Gly Thr Ser Asp Asp Thr Thr Pro Leu Arg
50 55 60

Ser Arg Val Thr Met Leu Val Asp Thr Ser Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Leu Ile Ala Gly Cys Ile Asp Val Trp Gly Gln Gly Ser
100 105 110

Leu Val Thr Val Ser Ser
115